

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/835,976

DATE: 05/08/2001
TIME: 15:55:17

Input Set : A:\PTO.txt
Output Set: N:\CRF3\05082001\I835976.raw

Does Not Comply
Corrected Diskette Needed

See pg 4-7

3 <110> APPLICANT: Mount, David B.
4 Delpire, Eric
5 Gamba, Gerardo
6 Alfred L. George, Jr.
8 <120> TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC ACIDS
AND
9 POLYPEPTIDES AND
10 THERAPEUTIC AND SCREENING METHODS USING SAME
12 <130> FILE REFERENCE: Attorney Docket No. 1242-26-2
14 <140> CURRENT APPLICATION NUMBER: US/09/835,976
15 <141> CURRENT FILING DATE: 2001-04-16
17 <160> NUMBER OF SEQ ID NOS: 131
19 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

4644 <210> SEQ ID NO: 16
4645 <211> LENGTH: 1150
4646 <212> TYPE: PRT
4647 <213> ORGANISM: Homo sapiens
4649 <220> FEATURE:
4650 <221> NAME/KEY: misc_feature
4651 <222> LOCATION: (35) ✓
4652 <223> OTHER INFORMATION: Xaa=Leu or Ile
4654 <220> FEATURE:
4655 <221> NAME/KEY: misc_feature /
4656 <222> LOCATION: (346)
4657 <223> OTHER INFORMATION: Xaa=Leu or Ile
4659 <220> FEATURE:
4660 <221> NAME/KEY: misc_feature /
4661 <222> LOCATION: (789)
4662 <223> OTHER INFORMATION: Xaa=Leu or Ile
4664 <400> SEQUENCE: 16
4665 Met His Pro Pro Glu Thr Thr Lys Met Ala Ser Val Arg Phe Met
4666 1 5 10 15
4668 Val Thr Pro Thr Lys Ile Asp Asp Ile Pro Gly Leu Ser Asp Thr Ser
4669 20 25 30
4671 Pro Asp Xaa Ser Ser Arg Ser Ser Arg Val Arg Phe Ser Ser Arg
4672 35 40 45
4674 Glu Ser Val Pro Glu Thr Ser Arg Ser Glu Pro Met Ser Glu Met Ser
4675 50 55 60
4677 Gly Ala Thr Thr Ser Leu Ala Thr Val Ala Leu Asp Pro Pro Ser Asp
4678 65 70 75 80
4680 Arg Thr Ser His Pro Gln Asp Val Ile Glu Asp Leu Ser Gln Asn Ser
4681 85 90 95
4683 Ile Thr Gly Glu His Ser Gln Leu Leu Asp Asp Gly His Lys Lys Ala
4684 100 105 110

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4686 Arg Asn Ala Tyr Leu Asn Asn Ser Asn Tyr Glu Glu Gly Asp Glu Tyr
 4687 115 120 125
 4689 Phe Asp Lys Asn Leu Ala Leu Phe Glu Glu Glu Met Asp Thr Arg Pro
 4690 130 135 140
 4692 Lys Val Ser Ser Leu Leu Asn Arg Met Ala Asn Tyr Thr Asn Leu Thr
 4693 145 150 155 160
 4695 Gln Gly Ala Lys Glu His Glu Glu Ala Glu Asn Ile Thr Glu Gly Lys
 4696 165 170 175
 4698 Lys Lys Pro Thr Lys Thr Pro Gln Met Gly Thr Phe Met Gly Val Tyr
 4699 180 185 190
 4701 Leu Pro Cys Leu Gln Asn Ile Phe Gly Val Ile Leu Phe Leu Arg Leu
 4702 195 200 205
 4704 Thr Trp Val Val Gly Thr Ala Gly Val Leu Gln Ala Phe Ala Ile Val
 4705 210 215 220
 4707 Leu Ile Cys Cys Cys Cys Thr Met Leu Thr Ala Ile Ser Met Ser Ala
 4708 225 230 235 240
 4710 Ile Ala Thr Asn Gly Val Val Pro Ala Gly Gly Ser Tyr Phe Met Ile
 4711 245 250 255
 4713 Ser Arg Ala Leu Gly Pro Glu Phe Gly Gly Ala Val Gly Leu Cys Phe
 4714 260 265 270
 4716 Tyr Leu Gly Thr Thr Phe Ala Ala Ala Met Tyr Ile Leu Gly Ala Ile
 4717 275 280 285
 4719 Glu Ile Phe Leu Val Tyr Ile Val Pro Arg Ala Ala Ile Phe His Ser
 4720 290 295 300
 4722 Asp Asp Ala Leu Lys Glu Ser Ala Ala Met Leu Asn Asn Met Arg Val
 4723 305 310 315 320
 4725 Tyr Gly Thr Ala Phe Leu Val Leu Met Val Leu Val Val Phe Ile Gly
 4726 325 330 335
 4728 Val Arg Tyr Val Asn Lys Phe Ala Ser Xaa Phe Leu Ala Cys Val Ile
 4729 340 345 350
 4731 Val Ser Ile Leu Ala Ile Tyr Ala Gly Ala Ile Lys Ser Ser Phe Ala
 4732 355 360 365
 4734 Pro Pro His Phe Pro Val Cys Met Leu Gly Asn Arg Thr Leu Ser Ser
 4735 370 375 380
 4737 Arg His Ile Asp Val Cys Ser Lys Thr Lys Glu Ile Asn Asn Met Thr
 4738 385 390 395 400
 4740 Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn Ser Ser Gln Phe Phe
 4741 405 410 415
 4743 Asn Ala Thr Cys Asp Glu Tyr Phe Val His Asn Asn Val Thr Ser Ile
 4744 420 425 430
 4746 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile Thr Glu Asn Leu Trp
 4747 435 440 445
 4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu Lys Pro Ser Ala Lys
 4750 450 455 460
 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu Tyr Val Leu Val Asp
 4753 465 470 475 480
 4755 Ile Thr Thr Ser Phe Thr Leu Leu Val Gly Ile Phe Phe Pro Ser Val
 4756 485 490 495
 4758 Thr Gly Ile Met Ala Gly Ser Asn Arg Ser Gly Asp Leu Lys Asp Ala

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4759 500 505 510
 4761 Gln Lys Ser Ile Pro Ile Gly Thr Ile Leu Ala Ile Leu Thr Thr Ser
 4762 515 520 525
 4764 Phe Val Tyr Leu Ser Asn Val Val Leu Phe Gly Ala Cys Ile Glu Gly
 4765 530 535 540
 4767 Val Val Leu Arg Asp Lys Phe Gly Asp Ala Val Lys Gly Asn Leu Val
 4768 545 550 555 560
 4770 Val Gly Thr Leu Ser Trp Pro Ser Pro Trp Val Ile Val Ile Gly Ser
 4771 565 570 575
 4773 Phe Phe Ser Thr Cys Gly Ala Gly Leu Gln Ser Leu Thr Gly Ala Pro
 4774 580 585 590
 4776 Arg Leu Leu Gln Ala Ile Ala Lys Asp Asn Ile Ile Pro Phe Leu Arg
 4777 595 600 605
 4779 Val Phe Gly His Ser Lys Ala Asn Gly Glu Pro Thr Trp Ala Leu Leu
 4780 610 615 620
 4782 Leu Thr Ala Ala Ile Ala Glu Leu Gly Ile Leu Ile Ala Ser Leu Asp
 4783 625 630 635 640
 4785 Leu Val Ala Pro Ile Leu Ser Met Phe Phe Leu Met Cys Tyr Leu Phe
 4786 645 650 655
 4788 Val Asn Leu Ala Cys Ala Leu Gln Thr Leu Leu Arg Thr Pro Asn Trp
 4789 660 665 670
 4791 Arg Pro Arg Phe Arg Tyr Tyr His Trp Ala Leu Ser Phe Met Gly Met
 4792 675 680 685
 4794 Ser Ile Cys Leu Ala Leu Met Phe Ile Ser Ser Trp Tyr Tyr Ala Ile
 4795 690 695 700
 4797 Val Ala Met Val Ile Ala Gly Met Ile Tyr Lys Tyr Ile Glu Tyr Gln
 4798 705 710 715 720
 4800 Gly Ala Glu Lys Glu Trp Gly Asp Gly Ile Arg Gly Leu Ser Leu Ser
 4801 725 730 735
 4803 Ala Ala Arg Phe Ala Leu Leu Arg Leu Glu Glu Gly Pro Pro His Thr
 4804 740 745 750
 4806 Lys Asn Trp Arg Pro Gln Leu Leu Val Leu Leu Lys Leu Asp Glu Asp
 4807 755 760 765
 4809 Leu His Val Lys His Pro Arg Leu Leu Thr Phe Ala Ser Gln Leu Lys
 4810 770 775 780
 4812 Ala Gly Lys Gly Xaa Thr Ile Val Gly Ser Val Ile Val Gly Asn Phe
 4813 785 790 795 800
 4815 Leu Glu Asn Tyr Gly Glu Ala Leu Ala Ala Glu Gln Thr Ile Lys His
 4816 805 810 815
 4818 Leu Met Glu Ala Glu Lys Val Lys Gly Phe Cys Gln Leu Val Val Ala
 4819 820 825 830
 4821 Ala Lys Leu Arg Glu Gly Ile Ser His Leu Ile Gln Ser Cys Gly Leu
 4822 835 840 845
 4824 Gly Gly Met Lys His Asn Thr Val Val Met Gly Trp Pro Asn Gly Trp
 4825 850 855 860
 4827 Arg Gln Ser Glu Asp Ala Arg Ala Trp Lys Thr Phe Ile Gly Thr Val
 4828 865 870 875 880
 4830 Arg Val Thr Thr Ala Ala His Leu Ala Leu Leu Val Ala Lys Asn Ile
 4831 885 890 895

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Input Set : A:\PTO.txt
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4833 Ser Phe Phe Pro Ser Asn Val Glu Gln Phe Ser Glu Gly Asn Ile Asp
4834 900 905 910
4836 Val Trp Trp Ile Val His Asp Gly Gly Met Leu Met Leu Leu Pro Phe
4837 915 920 925
4839 Leu Leu Lys Gln His Lys Val Trp Arg Lys Cys Ser Ile Arg Ile Phe
4840 930 935 940
4842 Thr Val Ala Gln Leu Glu Asp Asn Ser Ile Gln Met Lys Lys Asp Leu
4843 945 950 955 960
4845 Ala Thr Phe Leu Tyr His Leu Arg Ile Glu Ala Glu Val Glu Val Val
4846 965 970 975
4848 Glu Met His Asp Ser Asp Ile Ser Ala Tyr Thr Tyr Glu Arg Thr Leu
4849 980 985 990
4851 Met Met Glu Gln Arg Ser Gln Met Leu Arg His Met Arg Leu Ser Lys
4852 995 1000 1005
4854 Thr Glu Arg Asp Arg Glu Ala Gln Leu Val Lys Asp Arg Asn Ser Met
4855 1010 1015 1020
4857 Leu Arg Leu Thr Ser Ile Gly Ser Asp Glu Asp Glu Glu Thr Glu Thr
E--> 4858 025 1025 1030 1035 1040
4860 Tyr Gln Glu Lys Val His Met Thr Trp Thr Lys Asp Lys Tyr Met Ala
4861 1045 1050 1055
4863 Ser Arg Gly Gln Lys Ala Lys Ser Met Glu Gly Phe Gln Asp Leu Leu
4864 1060 1065 1070
4866 Asn Met Arg Pro Asp Gln Ser Asn Val Arg Arg Met His Thr Ala Val
4867 1075 1080 1085
4869 Lys Leu Asn Glu Val Ile Val Asn Lys Ser His Glu Ala Lys Leu Val
4870 1090 1095 1100
4872 Leu Leu Asn Met Pro Gly Pro Pro Arg Asn Pro Glu Gly Asp Glu Asn
E--> 4873 105 1105 1110 1115 1120
4875 Tyr Met Glu Phe Leu Glu Val Leu Thr Glu Gly Leu Glu Arg Val Leu
4876 1125 1130 1135
4878 Leu Val Arg Gly Gly Ser Glu Val Ile Thr Ile Tyr Ser
4879 1140 1145 1150
4882 <210> SEQ ID NO: 17
4883 <211> LENGTH: 712
4884 <212> TYPE: DNA
4885 <213> ORGANISM: Homo sapiens
4887 <400> SEQUENCE: 17
4888 agacaggaat ccgggttcgc ccctgcattcc tcctctgtt cacccttctg tcagtagtgt 60
E--> 4890 gggttatttt tt~~tttttttttt~~ gcatgtgcac ctttccacc agaccgaat ggattgtcga 120
4892 catcaaaaac accgggtggc tttgcataca cttcccccca gccagaccc tggttattc 180
E--> 4894 acctgata~~ca~~ caacaggtgg ccgggtgtac accttttagc aatctgatcc acgtatagt 240
4896 ccctgtataa aggtttgcct gcacgcatt ggcaccaacta gaaccctgg gacactcacc 300
4898 agataaaagga cttacctcga cagaaaaactg gggctgagg ggaggaggc ttcatctgt 360
4900 gcccctgagac catggcaactg agccctcagc cccggaccag aggggttagc taggttagtc 420
4902 ttcatctga agggaaagaag tcacacaaga ttggcattgt ttgttctttt tggtttttgt 480
4904 tttttctct cttaaaaaat atattcacct atgggtatg cacttcttag gacagtccgc 540
4906 ttgaattctg agtagaaata ttcttagttt gggcttgg tgggtgtga atcaaggta 600
4908 ttgaaatgtg ttattttca agttatctt tttattgcag taaaagtag ctacgtaaag 660
4910 aggaagattt tgcgagggttc ccccaactt tttgttctt aaaaagaaca aa 712

When numbering the
first amino acid on a
line, begin the
number directly under
the first letter of
the amino acid.

See item 10 on
Error summary
sheet

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Input Set : A:\PTO.txt
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4913 <210> SEQ ID NO: 18

4914 <211> LENGTH: 1014

4915 <212> TYPE: DNA

4916 <213> ORGANISM: mouse

4918 <400> SEQUENCE: 18

4919 tagccgcccgc ctccagctcc tttgccagga cgagacctct gggaggcagg aatccactct 60

4921 gcttcggcat cctctcgctgg ctctccttct ttccttctct gtagtgtggg ggtatttcc 120

4923 cgttatgcat ggcgcattctt cccaccagac ccaagtggtat tatcgaccc aaaaacatcg 180

4925 ggtggctcag cacacaccctc ctcccagcca gacctgtggg gtattcacct gatacacaac 240

4927 aggtggctgg tgcacaccc tgcgaatctt gatccacgtt ctttacgcg tggataagggt 300

4929 gggcctgcat gctccgtctt cagtagaaac cgtgggacac tcggcagata aaggactaac 360

4931 tacctcatcc ggaccctggg ggttggcag aggaggcgtt caccgtgc tttggatca 420

4933 tggcacggag cccacagccc tggaccaggag gagatagcta ggattctgaa agaaccaaagt 480

E--> 4935 tatacaggat tagcatcggtt ttgttcttat ttgttttctt cgaatttat ttttcagtttta 540 → item 10
4937 ctgggtgggc actttataaa acatcggtt tgaattctat acacgattt ttaattgggc 600
4939 ctttggggc tgtaaatcgat ggttaatttagt ggtttttgtt tttttttccc ctttcttatttt 660
4941 tgcacatcaga agtagctgtt gtaggaggaa gagtttttgtt gagttttcc tttttttttt 720
4943 gtcaaaaagg aaaggggggg gaaaatgcat ccaccagaag ccaccacca gatgtcctca 780
4945 gttcgggtca tggtgacacc aactaagattt gatgacattt caggttgc agacaccagc 840
4947 cccgacctca gctctcggtc tagttctcgat gtaagatttta gctccgaga aagtgtgcca 900
4949 gaaacaagcc gtagtgagcc tatgagcga ctgtctggg ctactacttc tctggcaact 960
4951 gttgcccttag atcctccag tgaccggact tctaattcccc agatgttac ggag 1014

4954 <210> SEQ ID NO: 19

4955 <211> LENGTH: 744

4956 <212> TYPE: DNA

4957 <213> ORGANISM: mouse

4959 <400> SEQUENCE: 19

4960 aagttagatgt ttcacctgaa ggaggagaga agcctttcac tgactcttgc aagggtttcc 60

4962 catatgcctt gaacttaagc aacaatggaa accgtccttt tttttcttga gttgacatag 120

4964 tgcctgtctt cattaaagag ggttagttgtt gaaataaaatgtt gttccctgtat ctttctcggt 180

4966 tgaagtaaaa ggacagatgt tgtagtaaggt tgagatgtt gaaaccagag aagtggcaat 240

4968 aaattaaagg aaacaatggg gagacacagg gtggacagttt ctttgcgttgc tcacgggctt 300

4970 tagctttctg ccgcctggag aaactgccc gacagtttga gttctacagg ttaataacaa 360

4972 taagctgggg tggagtgtt aagcccttta agagaatgtt aaacaggcg gaggcggtt 420

4974 ctcaagcgtt cccactccct tggggctat gtcacgtggg ctcagtttccc cccgattttcc 480

4976 acccactgttcccttagt gttctgtt gttggggg gaggaggcagg gacgcacggg 540

E--> 4978 aaggaaattt aaacgctgaa agcaagggtt gttttgtttaa aacaatgccc cacttcaactt 600 → item 10
4980 tgaccaaggtt agaagacccaa gaggaggggg cagctggccc cctctcttctt gggccatgtt 660
4982 cagcagaatgtt aaaaggccggg attcaggatc cccaaagacc aggttaatgtt gtcgtttgtt 720
4984 gcttcggggg accccacagac tagt 744

5321 <210> SEQ ID NO: 46

5322 <211> LENGTH: 315

5323 <212> TYPE: DNA

5324 <213> ORGANISM: Homo sapiens

5326 <400> SEQUENCE: 46

5327 gttggggcag agaaacatgg aggaggagca cacctgggtt gttcgtaatg atgaggactg 60

5329 cagagactgtt tgctggcctt cctggcaggc cccacgcattt ggcacccatc tggggctgtt 120

5331 cctggcgttcc ctgcagaaca tctttgggtt cttcccttcc ctgcgttgc cctgggttgg 180

5333 ggcatttgc ggcatttgc agtcccttcc catgggttttcc atctgttgc cctgtgttgg 240

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E--> 5335 tgacacccct cccctcacca cccctgaca gctggggctt ggcagaggcc tgg 300
 5337 gggtgggag gatgg 315
 6892 <210> SEQ ID NO: 113
 6893 <211> LENGTH: 361
 6894 <212> TYPE: PRT
 6895 <213> ORGANISM: Xenopus laevis
 6897 <400> SEQUENCE: 113
 6898 Arg His Glu Gly Thr Val Leu Leu Gly Asp Tyr Leu Asp Ser His Ala
 6899 1 5 10 15
 6901 Glu Ser Gln Ala Ala Glu Gln Ala Leu Lys His Leu Met Glu Gln Glu
 6902 20 25 30
 6904 Lys Val Lys Gly Phe Cys Gln Val Val Val Ala Gln Lys Leu Lys Glu
 6905 35 40 45
 6907 Gly Leu Ser His Leu Ile Gln Ser Cys Gly Leu Gly Gly Met Arg His
 6908 50 55 60
 6910 Asn Thr Val Ile Met Ser Trp Pro Ser Ser Trp Arg Gln Ser Asp Asp
 6911 65 70 75 80
 6913 Ser Arg Ala Trp Lys Ser Phe Ile Thr Thr Ile Arg Val Thr Thr Ala
 6914 85 90 95
 6916 Ala Arg Gln Ala Leu Leu Val Ala Lys Asn Val Ser Phe Phe Pro Gly
 6917 100 105 110
 6919 Ser Arg Glu Thr Leu Ala Glu Gly His Ile Asp Val Trp Trp Ile Val
 6920 115 120 125
 6922 His Asp Gly Gly Met Leu Met Leu Leu Pro Phe Leu Leu Lys Gln His
 6923 130 135 140
 6925 Lys Val Trp Arg Lys Cys Lys Met Arg Ile Phe Thr Val Ala Gln Met
 6926 145 150 155 160
 6928 Glu Asp Asn Ser Ile Gln Met Lys Lys Asp Leu Ala Thr Phe Leu Tyr
 6929 165 170 175
 6931 His Leu Arg Ile Ala Ala Asp Val Glu Val Val Glu Met His Asp Ser
 6932 180 185 190
 6934 Asp Ile Ser Ala Tyr Thr Tyr Glu Arg Thr Leu Met Met Glu Gln Arg
 6935 195 200 205
 6937 Ser Gln Met Leu Arg Gln Met Arg Leu Ser Lys Thr Asp Arg Glu Arg
 6938 210 215 220
 6940 Glu Ala Gln Leu Val Lys Asp Arg Asn Ser Ile Leu Arg Leu Thr Ser
 6941 225 230 235 240
 6943 Val Gly Ser Asp Asp Asp Glu Asp Thr Glu Ala Ala Pro Glu Arg Val
 6944 245 250 255
 6946 His Met Thr Trp Thr Arg Asp Lys His His Ala Val Arg Val Ala Gln
 6947 260 265 270
 6949 Ser Lys Pro Met Pro Ser Cys Gln Asp Leu Leu Asn Ile Arg Pro Asp
 6950 275 280 285
 6952 Gln Ser Asn Val Arg Arg Met His Thr Ala Val Lys Leu Asn Glu Val
 6953 290 295 300
 6955 Ile Val Asn Lys Ser His Asp Ala Lys Leu Val Leu Leu Asn Met Pro
 6956 305 310 315 320
 6958 Gly Pro Pro Arg Asn Pro Gln Gly Asp Glu Asn Tyr Met Glu Phe Leu
 6959 325 330 335

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E--> 6961 Glu Val Leu Thr Glu Gly Leu Glu Arg Val Leu Val Val Arg Gly Gly x
6962 340 345 350
6964 Gly Thr Glu Val Ile Thr Ile Tyr Ser
E--> 6965 355 360

O delete

FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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L:14 M:270 C: Current Application Number differs, Replaced Application Number
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:59 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:60 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:68 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:417 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:423 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:600 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:651 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:762 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:910 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:911 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:981 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:1062 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:1176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:1239 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1491 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1630 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1819 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1858 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1926 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1927 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:2062 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:2063 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:2510 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:2511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:2630 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:2631 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:2738 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:2739 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:2895 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:2982 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:3063 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:3143 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:3144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:3203 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:3204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11

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Input Set : A:\PTO.txt
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L:3343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:3344 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:3524 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:3569 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:4858 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
M:332 Repeated in SeqNo=16
L:4890 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17
M:340 Repeated in SeqNo=17
L:4935 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
L:4978 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:19
L:5335 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:46
L:6680 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:111
L:6808 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:112
L:6961 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:6961 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:6965 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:113
L:6965 M:252 E: No. of Seq. differs, <211>LENGTH:Input:361 Found:362 SEQ:113
L:7159 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:131